

FIG. 1

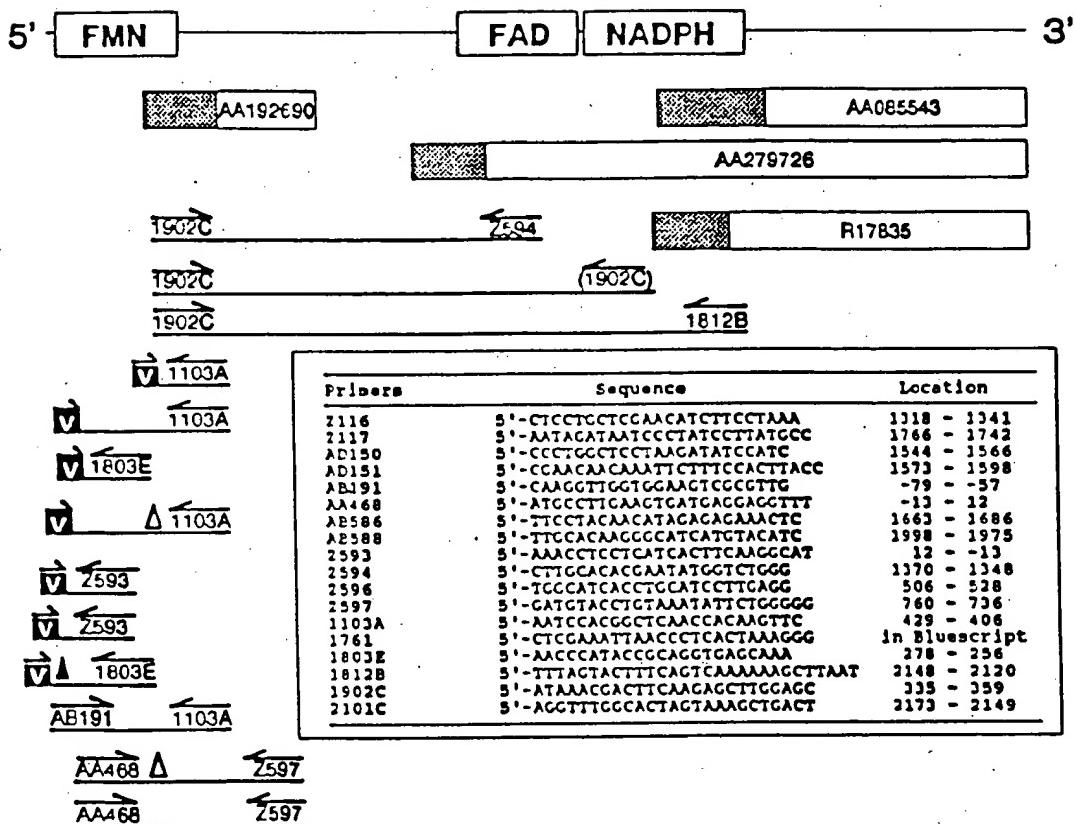


FIG. 2

1 ATGAGGAGGGTTCTGTACTATATGCTACACAGCAGGCCAGGGAAAGGCCATCGCACAGAACAAATGTGCAAGCTGTGCTACATGGATTTCTGCAGACATCTCACTGTATAGTCAA
 M R R F L L L Y A T O O G O K A A I E E M C E Q A V V H G F S A D L H C I S E 40
 121 TCCGATAAGTATGACCTAAAACCCAAACAGCTCTCTGTGTGCTTCTACCCAGGCCACGGGACAGGACCCACGCCACAGCGCAAGTTTGTAAGGAAATACAGAACAAACA
 S D K Y D L K T E T A P L V V V S T T G T G D P P D T A R K F V K E I G N O T 80
 241 CTGCGGGTTGATTCCTGTACTCCGCTATGGGTACTGGGCTCCGCTATTCAAGATAACACTACTTTGCAATGGGGGAAGATAAATTGATAAACGACTTCAAGAGCTTGGAGCC
 L P V D F F F A H K A R Y G L L G L G D S E T Y F C G M G K I I D K R L O E L G 120
 361 CGGCATTCTATGACACTGGCACATGCGAGTGTGAGGTTAAACTCTGGCTTCTGGCAGCTCTGGCAGGCCCTCAGAAAGCATTTAGTCAGCAGAGGACAA
 R H F Y D T G H A D D C V G L L V E P W I A G L W P A L R K H F R S S R G Q 160
 481 GAGGAGATAAGTGGGCCACTCCGGTGCATCACCTGCATCTTGAGGACAGACCTTGAGTCAGAGCTCTACACATTAACATCTCAAGTCAGCTTCTGAGATTCAGTCAAGGA
 E E I S G A L P V A S P A S L R T D L V K C S E L L H I E S O V E L L R F D D S 200
 601 AGAAAGGATTCTGAGGTTTGAAGCAAATGCACTGAAAGCAACCAATCCAATGTGTAATTGAAAGACTTTGAGTCTCTACACTTACCGTTGGTACCCCCACTCTCACAGCTCTG
 R K D S E V L K O N A V N S H O S N V I E D F E S S L T R S V P P L S O A S L 240
 721 AATATTCTCGTTTACCCCCAGAATATTACAGGTACATCTCCAGGAGTCTTGGCCAGGAGAAAGCCAAAGTATCTGACTTCAAGCAGTCAGTTTCAAGGCTTCAAG
 H I P G L P P E Y L O V H L O E S L G O E E S O V S V T S A D P V F O V P I S K 280
 841 CGAGTCAACTTACTACCAATGATGCCATAAAAACACTCTCTGGTACATTGACATTTCAAAACACACTTTCTATCAGCTGGAGATGCCCTCAGGGTATGCCCTAACAGT
 A V O L T H D A I K T T L V E L D I S H T D F S Y O P G D A F S V I C P N S 320
 961 GATTCAGCTACAAACGCTACTTCAAAAGACTCGAGCTGAAAGATAAAAGGACAGCTGGCTCTTGTAAATAAAAGGCAACACAAAGAAGAAAGGAGCTACCTTACCCAGCATATA
 D S E V O S L L O R L Q L E D K R E H C V L L K I K A D T K K G A T L P Q H I 360
 1081 CCTGCGGGATGTTCTCCAGTCACTTTTACCTGGTGTCTGAAATCCGAGCAATTCTAAAGGCAATTCTGGAGCCCTTGCGACTATACCTGAGCTGCTCAAAACGGCAGG
 P A G C S L Q F I T F W C L E I R A I P K K A F L R A L V D T T S D P V F O V P I S R 400
 1201 CTACAGGAGCTGGCACTAAACAGGGCACCCGATTATAGCCGCTTGTACAGGACATGCTTGGCTGTGTTCTGACTCTCCCTCGCTTTCCTCTGGCTTCCCTCTGGCAGCCACACTGAGTC
 L O E L C S K O G A A D Y S R F V R D A C A C L L D L L A F P S C O P P L S L 440
 1321 CTGCTCCAACATCTCTAAACTCTCAACCCAGACCATATTCTGTGCACTCAAGTATTCTACCCAGGAAAGCTCCATTGTTCTGACTCTCCCTCTGGCTTCCCTCTGGCACA
 L L E H L P K L O P R P Y S C A S S S L F H P G K L H F V F N I V E F L S T A T 480
 1441 ACAGAGGTTCTGGCAAGGGAGTATGACAGGTGGCTGGCTTGTGGTGTGCTCACTGCTTCAAGCAACACATGCTCCATGAAAGACACGGGGAAAGCCCTGGCTCTAACAGATA
 T E V L R K G V C T G W L A L L V A S V L O P N I H A S H E D S G K A L A P K I 520
 1561 TCCATCTCTCTCCAACAAACATTCTTCACTTACAGATGCCCTCAATCCCCTCATATACTGGCTGGCCAGAACCCGATAGCCCTTATGGGTTCTAACACATAGAGAC
 S I S P R T T N S F H L P D D P S I P I M V G P G T G I A P F I G F L O N R E 560
 1681 AAACCTCAAGAACACACCCAGATGAAATTCTGGAGCAATGTGGTGTGTTTGGCTCAGGATAAGGATAGGGATTATCTATTGAGAAAACAGCTCAGACATCTTCAACCATGG
 K L O E O H P D G M N F G A M H U L F F G G R H K D R O Y L F R K E L F H R L K H G 600
 1801 ATCTTAACCTCATCTAAAGGTCTCTCTCAAGAGATGTCTCTGTGGCCAGGAGCAAGGGCCAGAACAGTATGACACACACATCTGAGCTCATGCCAGGAGATCTCT
 I L T H L K V S F S R D A P V G E E E A P A K Y V O D N I Q L H G O O V A R I L 640
 1921 CTCCAGGAGAACGGCCATATTATGCTGGAGATGCCAAACATATGCCAAGGAGTGTACATGCTCCCTGTGCAAATAAAGCAAAGGCTGGAGTGAAGAAAACAGAACCAATG
 L O E N G H I T V C G D A K N H A K D V H D A L V O ' I S K E V G V E K L E A M 680
 2041. AAAACCTGGCACTTAAAGAAGAAAAACGCTACCTTCAGGATATTGCTATAAAACAGAAATTAAAGAAGAGGATTAAGCTTTTCACTGAAAGTACTAAAGTCAGCTTAC
 K T L A T L K E E K R Y L O D I V S *** 698

1 ATGAGGAGGTTCGTACTATGGTACACAGCAGGGACAGGAAAGGCCAACAGCTCCCTCTGGTGTGVVSYTTGTD
 M R R F L L Y A T Q G Q A K A E E M C E Q A V V H G F S A D L H C I S E 40
 S D K Y D L K T E T A P L V V R Y G L L G D S E Y T Y F C N G G K I I D K R L Q E L G A 120
 L P V D F F A H L R V V E P V I A G L W P A L R K H F R S S R G Q 160
 R H F Y D T G H A D D C V G L E L V V E P V I A G L W P A L R K H F R S S R G Q 160
 241 CTGGCGGTGATTCTTGTCACTGGGTATGGGTACTGGGTCGGTATTGAAATACACCTACTTGGTAATGGTAAAGGAAATA
 CGGATTAAGTATGCCAAAACGAAAGCTCCCTCTGGTGTGVVSYTTGTD
 361 CGGCATTCTATGACATGGACATGCCAGATGCGAGATGACTGTGAGGTAGGTTAGAAGCTGTGGTGAAGCTGGACTCTGGCC
 R H F Y D T G H A D D C V G L E L V V E P V I A G L W P A L R K H F R S S R G Q 200
 481 GAGGAGATAAAGTGGGCACTCCGGGGCATCACCTGGCATCCGTGAGCTGAGGAGACCCCTGAGGAGACGGTCAAGTCGAG
 E E I S G A L P V A S P A S L R T D L V K S E L L H I E S Q V E L L R F D D S G 200
 601 AGAAAGGATTCTGAGGTTTGAAGGCAAATGGAGTAAAGCACAATCCAATGGTAAATTGGAGACTTGTGAGATGGCTTACGGCT
 R K D S E V L K Q N A V N S N Q S N V V I E D F E S S L T R S V P P L S Q A S L 240
 721 AATATTCCGGTTAACCTGGGAGAACATTTACGGTACATCTGGAGGAGCTCTGGAGGAAAGCCAAAGTATCTGACTTCAGGAG
 N I P G L P P E Y L O V H L Q E S L G Q E E S Q V S V T S A D P V F Q V P I S K 280
 841 GGAGTTCACTTACTAGGAATGATGGCATTAAGGAACTTGCGTGGTAAATTGGGCAATTTCAGAGCTGGCTTACCCGGATATA
 A V Q L T T N D A I K T T L V E L D I S N T D F S Y Q O P G D A F S V I C P N S 320
 961 GATTCTGAGGTACAGCCACTCCAAAGACTGAGCTGAGCTGAGGAAATCCGGAAATCTGGAGGAACTGGGACTTACCCGGATATA
 D S E V Q S L L O R L Q L E D K R E H C V L L K I K A D T K K G A T L P Q H I 360
 1081 CCTGGGGATGTTCTCCAGTTCAATTGGGAAATTCGGGAAATCTGGGAGGAACTGGGCTTGGGACTTACCCGGGACCACITC
 P A G C S L Q F I F T W C L E I R A I P K K A F L R A L V D Y T S D S A E K R R 400
 1201 CTACAGGAGCTGTGAGTAACAAGGGCAGGATTAGCCGGTGTGAGGAGCTGGCTTGGGCTTGGGACTTACCCGGGACCACITC
 L Q E L C S K Q G A A D Y S R F V R D A C L L D L L A F P S C Q P P L S L 440
 1321 CTGCTGAGACATCTCTAAACTCAACCCAGACCATATCTGGTCAAGCTCAAGTTTACCCGGAAAGCTCCATTGGGAAATCTG
 L L E H L P K L O P R P Y S C A S S S L F H P G K L H F V F N I V E F L S T A T 480
 1441 ACAGGGTTCTGGAGGGAGTATGTCAGTTCTAGGCTGGCTGGCTGGGCTTGGGCTTGGGAGGCTTCTGGCTCTGGCT
 T E V L R K G V C T G W L A L L V A S V L O P N I H A S H E D S G K A L A P K I 520
 1561 TCCATCTCTCTCGAACACAACAAATTCTTCAAGGATGCTCCATCAATGCCCATCATATGGGGCATAGCCCCGTTATGGGT
 K L Q E Q H P D G N F G A M W L F F G C R H K D R D Y L F R K E L R H F L K H G 600
 1801 ATCTTAACATCTAAAGGTTCTCTCAAGGATGCTCCATCAAGGATGCTCCATCAATGCCCATCATATGGGGCATAGCCCC
 I L T H L K V S F S R D A P V G E E A P A K Y V Q D N I O L H G Q Q V A R I L 640
 1921 CTCAGGAGAACGGCCATATTATGTGTGGAGATGCAAGAAATAATGGCCAAGGTACATGATGCCCTGGCAAAATAATAG
 L Q E N G H I Y V C G D A K N M A K D V H D A L V Q I I S K E V G V E K L E A M 680
 2041 AAAACCTGGGCACCTTAAAGAAGAAAACGGTACCTTCAGGATATTGGCTAAAGACTAAAGTCGCTTAC
 K T L A T L K E E K R Y L Q D I W S *** 698

2161 TAGTGCCAAACCTTAAATTTCAACATTCTGAAAGGACATGGAGTGGAGATTGATCTTCAACAAATAACAAACACTTCY
 2281 TTCTATCTACGCCCTTCTGCGCTGACTCTCCAAATTGCCCTGCTTGGCTTGGCTTAAGGCAAGCTTCGCTTACTCCCGAGA
 2401 TCAGAGAGACTCTGCTCCATGCAAGGGCTCTCTGAAATAGGGAGACTGACTGAGTGGCTTACATGAGCTTAAATGGTT
 2521 TAGATGATATACCCAAAGAATGCTCAATTATGTTGACTAAATGAGCTTAAATGGTCAATCTGTTAAGCTTAAATGG
 2661 ATAAAAAATATTATGGGAGGATTATTCTGAGGATGCTGAGGTTTAAATAGAAAGTACACCTTAAATGGGAGGATT
 2761 TTAAAGTCACCATTCAGATTCTGAGATTCTGAGCTTAAATGGGAGGATTATTCTGAGGTTTAAATGGGAGGATT
 2881 GGACATTTTGGTACCTTCAGGATTTCTGAGCTTAAATGGGAGGATTATTCTGAGGTTTAAATGGGAGGATT
 3001 TCCCTGTTAATTGCAACAAACAAATGTTATGATACTTCTGACTTAAACACTCTGTTGAGGCTTAAACACTCTGTT
 3121 TGATCCCTTGTGAGAAAATGATGCAAAAGATGCAAGAAAATGATGCAAAAGATGCAAGAAAATGATGCAAAAGATGCA

HsMTRR	-----		
CeMTRR	-----		
HsCPR	HGDSHVGTSSTVSEAVAEVSLFSMTDMILFSLIVGLLTWFLFRKKKEE	50	
	FMN		
HsMTRR	-----MARRFLLLTATGCCCAKATAEEMCE	24	
CeMTRR	-----MTOFLIAFCSCITCCAETIAKSLKE	24	
HsCPR	VFEFTKIGTLTSSVRESSFVEKMKKTGRNIVFYGSGOTGTAEEFAHRLSK	100	
	FMN		
HsMTRR	CAVVHGCSAQLHCISESDK-YDLKT-----ETAPLVVVVSITGTCGPP	66	
CeMTRR	KAELIGLTFRLHALDENNEKKFHLINE-----EXLC-AIVVSSSTGGGAP	66	
HsCPR	DAHRTG----MRGMSADPEEYDADLSSLPEIDNALVVFCHMAYCEGOPT	146	
	FMN		
HsMTRR	CTAARFVKEICHTLPVDFFAHLRTGGLGCGSEYYTFCGGRGTTCKRLO	116	
CeMTRR	ENCAAFVFRINRNSLENEYLKNDYVLLGCGSNSYYGTIFRKIDKLT	116	
HsCPR	ENACQDFYDULCETQVD---LSCGVKFAVFLGCHKTYEHFNAMGKRYVKERLE	193	
	FMN		
HsMTRR	ELGARHYDTGHADDCCVGLELVEEPWIAGLWFALRKHFRRSSRCOEISGA	166	
CeMTRR	ALGAKRLIDRAEAADDCCVGLEEVEPWIKEKFATLASRFDISADKHM----	162	
HsCPR	OLGAGRIEFLCLGCGCGNLLEDFITURECFWPAVCENF-----GV	233	
	FMN		
HsMTRR	LFVASPASLRDOLVKSELLHIESCVELL--RFDCSGRKEDSEVLKCHAVNS	214	
CeMTRR	-AITESENKLKNCVKTE---EKKALLCKRIEDEESDDEGCRGVICID-	206	
HsCPR	EATGELESS;FCYEL-----VVNTDIDAAKVYHGENGRKYSTEN	271	
	FMN		
HsMTRR	MCSNVVIEDF---ESSLTRSVPPPLS-CASLNIPGLPPEYLOVNLCESLCO	260	
CeMTRR	---MLIPEHYDYPEISSLKGSQTLSDENLRVPJAPGPFIVSSVSNEKLP	253	
HsCPR	CKP-----FFD-----AKNPFLAAVTINKLN	293	
	FMN		
HsMTRR	EEECVS-----VTSADPVFCVPISKAVOLTT--NDAIKTLLVELDIS	301	
CeMTRR	ECTXLEWCNLCKMPGCVTKFEEVLVSAEFVTDPSKIKTKRMITVDFG	303	
HsCPR	GCTE-----RNLMHLELD	306	
	FMN		
HsMTRR	N---TDFSTOFCCAFSVICPHNSDSEVCSLLOR-LOLEDKREMVLLKIKAD	348	
CeMTRR	CHAAELCTEFCDAAITFCVFPNALEVNFIILKRCVGVLDDIADOCCEL-SINPK	352	
HsCPR	ISCSKIRTESGCHAVVYPAANDSALVNOLGX---ILGADLD--VVMSLHNLL	351	
	FMN		
HsMTRR	TKKKCATLPCNIPACCSSLIFIITUCLEIRAIPIKKAFLRALVDTTSDSAEK	398	
CeMTRR	TEKINACIPCHVHKITLFLHNNFTICLDIRAPGRPLIRVLAESTSDOFNEK	402	
HsCPR	DEESENXXHP---/PCPTSYTIALTYLDITHPPRTNVLYELACTASEFSEQ	399	
	FMN		
HsMTRR	RRLOEL--CSKCGAACDYSRFVRDACAICLDDLLAFAFPSCOPPLSLEHLP	446	
CeMTRR	FRLLEL--CSACGHHDFDFVTPGCLSLADMLFAFPNVKPPVDRLLIELLP	450	
HsCPR	ELLRKHASSSEGGKELYLSUVVEARHILALILOCPSLRFPIHDLCLELP	449	
	FAD		
HsMTRR	KLCFPTSCASSSLFHFGKLMHFVFNIVEFLSTATIEVLRKGQVETGWALL	496	
CeMTRR	FLTRPFYSHSS---YENKXARLITSENEFPAFDGRRHSRKGLATDULHNSL	497	
HsCPR	RLCARTTYSIASSSKVHPNSVRICAVVETETKAGR--INKQVATNUL---	496	
	FAD		
HsMTRR	VASVLOPNIHASHEDSGKALAKP1S1SPRTINSFHLR-----DDPSITP	539	
CeMTRR	R-----IGDKVQVVLGEFARFLRPLPGMTKNSACKLP	529	
HsCPR	RAKE-----PVCENGGRALVPMFVRKSOFRLPK-----ATTIP	527	
	NADPH		
HsMTRR	IIMVPGCTGIAFFIGFLCHREKLCOEONPOGNFGAMW-LFFGCCRHKDRDTL	588	
CeMTRR	LLMVGPCITGVSFELSFLFLRKLKDGSFSDFDVDPVRVLFGCROSSVDAL	579	
HsCPR	VIMZGCTGVAFFIGFIQERAVLRCGKKE---VGETLLYTGCRSDEDYL	574	
	NADPH		
HsMTRR	FRKELRHFLXHGCLTLLKVSFSRDAFVGEEEPAFKYVODNIOLNGOCVAR	638	
CeMTRR	YHSELEMVFSEGILTDLICESEQ-----XGERVCDGLRKYLDEKLP	621	
HsCPR	YREELACFHRODGALTOLNVAFSRE---OSHKVYVOHLLKODREHLWK	618	
	NADPH		
HsMTRR	TLLOE-NGHITVCGOAKNHAKDVKHDALVQIIISKEVGVEKLEAKTLATLK	687	
CeMTRR	FLTASTESKIFCCDAKCSKDVKWCFSDIVASDOCIPDLEAKKLHDLK	671	
HsCPR	L1--EGGAHIIVCCGDAHNRDVCNTFYDIAELGAMEHAOVDYIKLM	666	
	NADPH/FAD		
HsMTRR	EKRYLQDWS 698		
CeMTRR	KSDOYIEDWQ 682		
HsCPR	TKGRYLSDWJS 677		

HsMTRR	MGGCQVDTSSVSEAVAEVEVSLFSMTDMILFLSILVGLLTYWFLKKKKE	50
CeMTRR	-----MRRFLLLYATDQGQAKAJAEMCE	24
HsCPR	-----MTDFLIAFGSGTGOAETIASKLKE	24
	VPEFTKIOTLTSSVRESSFVEKMKTGRNIIVFYGSOTGTAAEFAFNRLSK	100
	FMN	
HsMTRR	QAVVHGFSADLHCISESDK-YDLKT-----ETAPLVVVVSTTGTGDPP	66
CeMTRR	KAELIGLTPRLHALDENEKKFNLNE-----EKLC-AIVVSTGDDGAP	66
HsCPR	DAHRYG---MRGMSADPEEYDADLSSLPEIDNALVVFCMATYEGDPT	146
	FMN	
HsMTRR	DTARKFVKIEONOTLPVDFFAHLRYGLGLGDSEYYTFCHNGKIIDKRLO	116
CeMTRR	DNCARFVRRINRNSLENEYLKNLDYVLLGLGDSNYSYOTIPRKIDKOLT	116
HsCPR	DNAODFYDWLQETDVD---LSGVKFAVGLGNKTYEHFNAMGKVVDKRE	193
	FMN	
HsMTRR	ELGARHFYDTGHADDVGLELVVEPWIAGLWPALRKHFRRSSRGEEISGA	166
CeMTRR	ALGANRLFDRAEADDOVGLELEVPIEKFATLASRFDISADKMN---	162
HsCPR	OLGAORIFELGLGDDGNLEEDFITWREOFWPACVEHF-----GV	233

HsMTRR	LPVASPASLRDVLKSELLHIESOVELL--RFDDSGRKDSEVLKONAVNS	214
CeMTRR	-AI TEESNLKLNOVKT-----EEKKALLOKRIEDEESDDEGRGRVIGID-	206
HsCPR	EATGEESSIROYEL-----VVHTDIDA KAVYMGEMGRLKSYEN	271

HsMTRR	NCSNVIEDF---ESSLTRSVPPPLS-QASLNIPGLPPEYLOVHLOESLGQ	260
CeMTRR	--MLIPEHYDYPEISLLKGSQLTSNDENLRVPIAPOFPFIVSSVNRKLP	253
HsCPR	OKP-----PFD-----AKNPFLAAVTNRKLN	293

HsMTRR	EESOVS-----VTSADPVFCVPISKAVQLT--NDAIKTTLLVELDIS	301
CeMTRR	EDTKLEWNLCMKPGVVTKPFEVLLVSAEFVTDPSKIKTKRMITVDFG	303
HsCPR	QGTE-----RHLMHLELD	306

HsMTRR	N--TDFSYOPGDAFSVICCPNSDSEVOSLLOR-LOLEDKREHCVLLKIKAD	348
CeMTRR	DHAELOYEPGDAIYFCVPNPALEVNFILKRCGVLDIADQOCCEL-SINPK	352
HsCPR	ISDSKIRYESGDHVAVYPANDSALVNOLGK---ILGADL--VMSLNLL	351

HsMTRR	TKKKGATLPCOHIPAGC5L0FIFTWCLERAIKPKAFLRALVDYTSDSAEC	398
CeMTRR	TEKINAQ1PCGHVHKITTLRHMFTTCLDIRRAPGRPLIRVLAESTSDPNEK	402
HsCPR	DEESNNKHP--FPCPTSYRTALTYLDITNPPTTNVLYELAQYASEPSEQ	399

HsMTRR	RRLOEL--CSKOGAADYSRFVRDACA CLD LLLA F PSCOPPLS LL E HLP	446
CeMTRR	RRLIEL--CSAOGMKGDFTDVFRTPGLS LADML F A FP NVKPPVDR LI ELLP	450
HsCPR	ELL RMA SSS GEG KELYLSW V V E A R R H I L A I L O D C P S L R P P I D H L C E L L P	449

HsMTRR	KLOPRPYSCASSSLFHPGKLHVFVNIVFELSTATTEVLRKGVCTGWALL	496
CeMTRR	RLI P R P Y S M S S -- Y E N R K A R L I Y S E M E F P A T D G R R H S R K G L A T D W L N S L	497
HsCPR	RLOARYYSIASSSKVHPNSVHICAVVVEYETKAGR--INKGVATNWL--	494

HsMTRR	VASVLOPNIHASHEDSGKALAPKISPRTTNSFHLP-----DDPSIP	539
CeMTRR	R-----IGDKVOVLGKEPARFLPPLGMTKNSACKLP	529
HsCPR	RAKE-----PVGENGGRALVPMFVRKSQFRLPFK-----ATT P	527
	*	
	<u>NADPH</u>	
HsMTRR	IIMVGP GTI A P F I G F L O H R E K L Q E O H P D G N F G A M W - L F F G C R H K D R D Y L	588
CeMTRR	L L M V G P G T G V S V F L S F L H F L R K L K Q D S P S D F V D V P R V L F F G C R D S S V D A I	579
HsCPR	VIMVGP GTVAPF I G F I Q E R A W L R Q Q G K E -- V G E T L L Y G C R R S D E D Y L	574

	<u>NADPH</u>	
HsMTRR	FRKELRHF LKH G I L T H L K V S F S R D A P V G E E E A P A K Y V D N J Q L H Q Q O V A R	638
CeMTRR	Y M S E L E M F V S E G I L T D L I C E S E O ----- K G E R V D G L R K Y L D K V L P	621
HsCPR	Y R E E L A Q F H R D G A L T O L N V A F S R E ----- Q S H K V V Q H L L K O D R E H L W K	618

	<u>NADPH</u>	
HsMTRR	I L Q E - N G H I Y V C G D A K N M A K D V H D A L V O I I S K E V G V E K L E A M K T L A T L K	687
CeMTRR	F L T A S T E S K I F I C G D A K G M S K D V W O C F S D I V A S D O G I P D L E A K K L M D L K	671
HsCPR	L I -- E G G A H I Y V C G D A R N M A R D V O N T F Y D I V A E L G A M E H A Q A V D Y I K K L M	666

	<u>NADPH/FAD</u>	
HsMTRR	E E K R Y L O D I W S 698	
CeMTRR	K S D Q Y I E D V W G 682	
HsCPR	T K G R Y S L D V W S 677	

FIG. 4

FIG. 5A

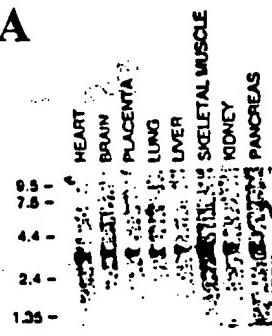


FIG. 5B



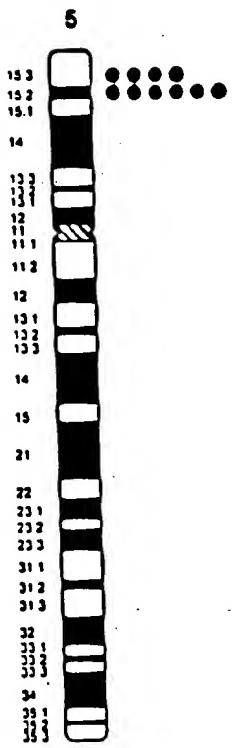


FIG. 6

FIG. 7A



FIG. 7B

FIG. 7C

Position	Sequence	Accessions	Protein	Organism
972	CAPVLLYFCCHHFDWVWLY	[AF025794]	WTBP	[H. sapiens]
958	CETLILYYCCPPSDENLY	[AAU557]	CPR	[H. sapiens]
959	CETLILYYCCPRAAEDLY	[DQ0101]	CPR	[O. cuniculus]
960	CESILLYFCCPRAECDVLY	[JGI490]	CPR	[D. melanogaster]
972	CPALLLFFCCCHPCHDPLV	[P37114]	CPR	[V. radiata]
573	CPTVLLFFGCCHPSEDPLV	[Z2A438]	CPR	[A. niger]
1281	CPTVLLFFGCCHPSEDPLV	[D19408]	NOS	[H. sapiens]
1281	CPTVLLYFCCPSPSFLVLY	[UG0610]	NOS	[H. sapiens]
1009	CPNTLIVFCCPPTEDMLV	[U02610]	NOS	[H. sapiens]
1040	CPNTLIVFCCPPSQDMLV	[L24910]	NOS	[H. sapiens]
380	CPNTLIVFCCPHSQDMLV	[U05091]	NOS	[H. sapiens]
1005	CDTLLILYCCPHCNDRLY	[U05091]	NOS	[H. sapiens]
481	CPNWLIVFCPHTTEDPLV	[M21008]	SP	[S. cerevisiae]
915	CEVFLIVFCPHTTEDPLV	[U05091]	SP	[S. cerevisiae]
407	CEVFLIVFCPHTTEDPLV	[Z31149]	SP	[S. pombe]
241	CLAVLIFLCVANTUSLLVD	[X52419]	PRR	[S. cerevisiae]
241	CLAVLIFLCVANTUSLLVF	[P00455]	PRR	[S. cerevisiae]

FIG. 8A

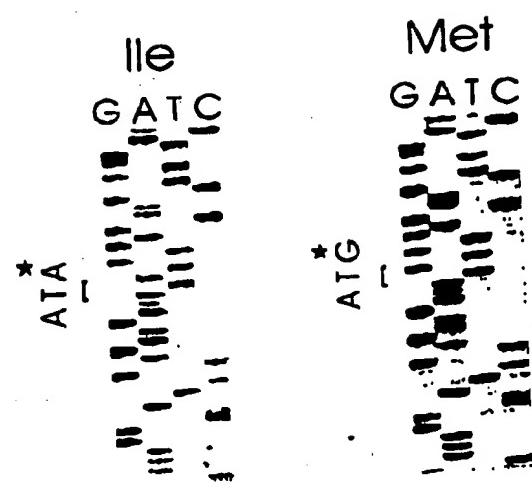


FIG. 8B

